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☐ 1: NP_115972. ATP-binding casse...[gi:21729873]

Links

LOCUS ABCC11 1382 aa linear PRI 05-NOV-2002

DEFINITION ATP-binding cassette, sub-family C, member 11 isoform a;
multi-resistance protein 8; ATP-binding cassette transporter MRP8;
ATP-binding cassette protein C11 [Homo sapiens].

ACCESSION NP_115972

VERSION NP_115972.2 GI:21729873

DBSOURCE REFSEQ: accession NM_032583.2

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (residues 1 to 1382)

AUTHORS Dean,M., Rzhetsky,A. and Allikmets,R.

TITLE The human ATP-binding cassette (ABC) transporter superfamily

JOURNAL Genome Res. 11 (7), 1156-1166 (2001)

MEDLINE 21329047

PUBMED 11435397

REFERENCE 2 (residues 1 to 1382)

AUTHORS Tammur,J., Prades,C., Arnould,I., Rzhetsky,A., Hutchinson,A.,
Adachi,M., Schuetz,J.D., Swoboda,K.J., Ptacek,L.J., Rosier,M.,
Dean,M. and Allikmets,R.

TITLE Two new genes from the human ATP-binding cassette transporter
superfamily, ABCC11 and ABCC12, tandemly duplicated on chromosome
16q12

JOURNAL Gene 273 (1), 89-96 (2001)

MEDLINE 21376129

PUBMED 11483364

REFERENCE 3 (residues 1 to 1382)

AUTHORS Bera,T.K., Lee,S., Salvatore,G., Lee,B. and Pastan,I.

TITLE MRP8, a new member of ABC transporter superfamily, identified by
EST database mining and gene prediction program, is highly
expressed in breast cancer

JOURNAL Mol. Med. 7 (8), 509-516 (2001)

MEDLINE 21475973

PUBMED 11591886

REFERENCE 4 (residues 1 to 1382)

AUTHORS Yabuuchi,H., Shimizu,H., Takayanagi,S. and Ishikawa,T.

TITLE Multiple splicing variants of two new human ATP-binding cassette
transporters, ABCC11 and ABCC12

JOURNAL Biochem. Biophys. Res. Commun. 288 (4), 933-939 (2001)

MEDLINE 21547789

PUBMED 11688999

COMMENT REVIEWED REFSEQ: This record has been curated by NCBI staff. The
reference sequence was derived from AF367202.1.
On Jul 11, 2002 this sequence version replaced gi:14211905.
Summary: The protein encoded by this gene is a member of the

superfamily of ATP-binding cassette (ABC) transporters. ABC proteins transport various molecules across extra- and intra-cellular membranes. ABC genes are divided into seven distinct subfamilies (ABC1, MDR/TAP, MRP, ALD, OABP, GCN20, White). This ABC full transporter is a member of the MRP subfamily which is involved in multi-drug resistance. It is expressed at low levels in all tissues, except kidney, spleen, and colon. This gene and family member ABCC12 are determined to be derived by duplication and are both localized to chromosome 16q12.1. Their chromosomal localization, potential function, and expression patterns identify them as candidates for paroxysmal kinesigenic choreoathetosis, a disorder characterized by attacks of involuntary movements and postures, chorea, and dystonia. Multiple alternatively spliced transcript variants have been described for this gene. Transcript Variant: This variant (1), as well as variant 2, encodes the predominant isoform (a).

FEATURES

source

Location/Qualifiers

1..1382

/organism="Homo sapiens"

/db_xref="taxon:9606"

/chromosome="16"

/map="16q12.1"

Protein

1..1382

/product="ATP-binding cassette, sub-family C, member 11 isoform a"

/note="multi-resistance protein 8; ATP-binding cassette transporter MRP8; ATP-binding cassette protein C11"

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/note="ABC_membrane"

/db_xref="CDD:pfam00664"

Region

536..691

/region_name="ATPases associated with a variety of cellular activities"

/note="AAA"

/db_xref="CDD:smart00382"

Region

537..708

/region_name="ABC transporter. ABC transporters for a large family of proteins responsible for translocation of a variety of compounds across biological membranes. ABC transporters are the largest family of proteins in many completely sequenced bacteria. ABC transporters are composed of two copies of this domain and two copies of a transmembrane domain pfam00664. These four domains may belong to a single polypeptide or belong in different polypeptide chains"

/note="ABC_tran"

/db_xref="CDD:pfam00005"

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/region_name="ABC transporter transmembrane region. This family represents a unit of six transmembrane helices. Many members of the ABC transporter family (pfam00005) have two such regions"

/note="ABC_membrane"

/db_xref="CDD:pfam00664"

Region

1168..1360

/region_name="ATPases associated with a variety of

cellular activities"

/note="AAA"

/db_xref="CDD:smart00382"

Region

1169..1351

/region_name="ABC transporter. ABC transporters for a large family of proteins responsible for translocation of a variety of compounds across biological membranes. ABC transporters are the largest family of proteins in many completely sequenced bacteria. ABC transporters are composed of two copies of this domain and two copies of a transmembrane domain pfam00664. These four domains may belong to a single polypeptide or belong in different polypeptide chains"

/note="ABC_tran"

/db_xref="CDD:pfam00005"

CDS

1..1382.

/gene="ABCC11"

/coded_by="NM_032583.2:79..4227"

/note="transporter"

/db_xref="LocusID:85320"

/db_xref="MIM:607040"

ORIGIN

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481 lswqqtcpqi vngalelern ghasegmtrp rdalgpeeeeg nslgpelhki nlvsvskgmml
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1381 lr
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Revised: July 5, 2002.

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Oct 31 2002 16:00:17

FASTA searches a protein or DNA sequence data bank
version 3.3t05 March 30, 2000
Please cite:
W.R. Pearson & D.J. Lipman PNAS (1988) 85:2444-2448

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>SEQ ID NO 23 human transporter
vs /tmp/fastadaadZaWfX library
searching /tmp/fastadaadZaWfX library

1382 residues in 1 sequences

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join: 40, opt: 28, gap-pen: -12/ -2, width: 16
Scan time: 0.050

The best scores are: opt

gi|21729873|ref|NP_115972.2| ATP-binding cassette (1382) 4838

>>gi|21729873|ref|NP_115972.2| ATP-binding cassette, sub (1382 aa)
initn: 7928 init1: 4838 opt: 4838

Smith-Waterman score: 7606; 88.061% identity in 1382 aa overlap (1-1219:1-1382)

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gi 217	MTRKRTYWVPNSSGGLVNRGIDIGDDMVSGLIYKTYTLQDGPWSQQERNPEAPGRAAVPP					
	10	20	30	40	50	60
	70	80	90	100	110	120
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gi 217	WGKYDAALRTMIPFRPKPRFPAPQPLDNAGLFSYLTVSWLTPLMIQSLRSRLDENTIPPL					
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	130	140	150	160	170	180
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gi 217	SVHDASDKNVQRLHRLWEEVSRRGIEKASVLLVMLRFQTRLIFDALLGICFCIASVLG					
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	190	200	210	220	230	240
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gi 217	PILIIPKILEYSEEQLGNVVHGVGLCFALFLSECVKSLSFSSSWIINQRTAIRFRAVSS					
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	250	260	270	280	290	300
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gi 217	FAFEKLIQFKSVIHITSGEAISFFTGDVNYLFEGVCYGPLVLITCASLVICSISSEYFIIG					
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	310	320	330	340	350	360
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	370	380	390	400	410	420
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      490      500      510      520      530      540
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      550      560      570      580      590      600
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gi|217 GVCGNTGSGKSSLLSAILEEMHLLGSGVGVQGSLAYVPQQAWIVSGNIRENILMGGAYDK
      550      560      570      580      590      600

      610      620      630      640      650      660
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      670      680      690      700      710      720
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      730
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      730      740      750      760      770      780

      790      800      810      820      830      840
SEQ    -----
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      850      860      870      880      890      900
SEQ    -----
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      910      920      930      940      950      960
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      910      920      930      940      950      960

      970      980      990      1000      1010      1020
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      920      930      940      950      960      970
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```

      1160      1170      1180      1190      1200      1210
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Function used was FASTA